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Yvonne Mock

PATENT
Attorney Docket No.: 020547-003560US
Client Ref. No.: 010080.06

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Confirmation No. 3275
Bryan JULIEN et al.	Examiner: Hope A. Robinson
Application No.: 10/729,802	Art Unit: 1656
Filed: December 5, 2003	AMENDMENT
For: DISORAZOLE POLYKETIDE SYNTHASE ENCODING POLYNUCLEOTIDES	
Customer No.: 20350	

Mail Stop Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

In response to the Office Action mailed June 7, 2006, please enter the following amendments and remarks:

Amendments to the Title begin on page 2 of this paper.

Amendments to the Specification begin on page 3 of this paper.

Amendments to the Claims are reflected in the listing of claims which begins on page 5 of this paper.

Remarks/Arguments begin on page 7 of this paper.

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Amendment to the Title:

Please replace the Title on page 1, with the following amended Title:

POLYNUCLEOTIDES ENCODING
DISORAZOLE POLYKETIDE SYNTHASE POLYPEPTIDES
~~ENCODING POLYNUCLEOTIDES~~

Please replace paragraph [0037] with the following amended paragraph:

[0037] In one aspect, the invention provides a polynucleotide comprising a sequence identical or substantially identical SEQ ID NO: 1 or its complement, or to a portion of SEQ ID NO: 1 or its complement encoding a domain, module, ORF, or region (e.g., as shown in Table 1). (Reference herein to SEQ ID NO:1 will be understood to refer also to the complementary nucleic acid sequence, except where clear from context that reference to a particular strand in intended.) In one aspect, the invention provides a polynucleotide comprising a sequence identical or substantially identical a fragment of SEQ ID NO:1 described in the Examples, infra, or a sequencing variant of SEQ ID NO: 1 described in the Examples, or a portion thereof encoding a domain, module, ORF, or region. As used in this context, two nucleic acid sequences (or two polypeptide sequences) are substantially identical if they have at least about 70% sequence identity, often at least about 80%, at least about 90%, at least about 95%, or even at least about 98% sequence identity. A degree of sequence identity can be determined by conventional methods, e.g., Smith and Waterman, 1981, Adv. Appl. Math. 2:482, by the search for similarity method of Pearson & Lipman, 1988, Proc. Natl. Acad. Sci. USA 85:2444, using the CLUSTAL W algorithm of Thompson et al., 1994, Nucleic Acids Res 22:467380, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. The BLAST algorithm (Altschul et al., 1990, Mol. Biol. 215:403-10) for which software may be obtained through the National Center for Biotechnology Information (~~http://~~www.ncbi.nlm.nih.gov/) can also be used. When using any of the aforementioned algorithms, the default parameters for "Window" length. gap penalty, etc., are used. It will be appreciated that a reference to a DNA sequence is also a reference to the reverse complement of that sequence (e.g., the sequence of the complementary DNA strand).

Please replace paragraph [0091] with the following amended paragraph:

[0091] The relationships of the clone inserts are shown in Figure 2. Sequences characteristic of KS domains were identified in each of the clones, as indicated. The "CSSSL" motif (SEQ ID NO:10) characteristic of KS domains was found in the partially sequenced KS domains of pKOS254-190.1 and pKOS254-190.2. Interestingly, sequence analysis of pKOS254-190.7 revealed a ketosynthase (KS) domain adjacent to a dehydrogenase (DH) domain, with no intervening actyl transferase (AT) domain. This suggested that the AT activity is supplied by an AT encoded as a separate protein, rather than existing as domains in each of several modules.